

SEQUENCE LISTING

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Mark J. Graham
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<120> ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN
EXPRESSION

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cctgataacc atg ctg gct gcc aca gtc ctg acc ctg gcc ctg ctg ggc 169
Met Leu Ala Ala Thr Val Leu Thr Leu Ala Leu Leu Gly
1 5 10

aat gcc cat gcc tgc tcc aaa ggc acc tcg cac gag gca ggc atc gtg 217
Asn Ala His Ala Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val

15	20	25	
tgc cgc atc acc aag cct gcc ctc ctg gtg ttg aac cac gag act gcc			265
Cys Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu Thr Ala			
30 35 40 45			
aag gtg atc cag acc gcc ttc cag cga gcc agc tac cca gat atc acg			313
Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser Tyr Pro Asp Ile Thr			
50 55 60			
ggc gag aag gcc atg atg ctc ctt ggc caa gtc aag tat ggg ttg cac			361
Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His			
65 70 75			
aac atc cag atc agc cac ttg tcc atc gcc agc agc cag gtg gag ctg			409
Asn Ile Gln Ile Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu			
80 85 90			
gtg gaa gcc aag tcc att gat gtc tcc att cag aac gtg tct gtg gtc			457
Val Glu Ala Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val			
95 100 105			
ttc aag ggg acc ctg aag tat ggc tac acc act gcc tgg tgg ctg ggt			505
Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Trp Leu Gly			
110 115 120 125			
att gat cag tcc att gac ttc gag atc gac tct gcc att gac ctc cag			553
Ile Asp Gln Ser Ile Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln			
130 135 140			
atc aac aca cag ctg acc tgt gac tct ggt aga gtg cgg acc gat gcc			601
Ile Asn Thr Gln Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala			
145 150 155			
cct gac tgc tac ctg tct ttc cat aag ctg ctc ctg cat ctc caa ggg			649
Pro Asp Cys Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly			
160 165 170			
gag cga gag cct ggg tgg atc aag cag ctg ttc aca aat ttc atc tcc			697
Glu Arg Glu Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser			
175 180 185			
ttc acc ctg aag ctg gtc ctg aag gga cag atc tgc aaa gag atc aac			745
Phe Thr Leu Lys Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn			
190 195 200 205			
gtc atc tct aac atc atg gcc gat ttt gtc cag aca agg gct gcc agc			793
Val Ile Ser Asn Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser			
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Ile Leu Ser Asp Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp			
225 230 235			
ccc gtc atc aca gcc tcc tac ctg gag tcc cat cac aag ggt cat ttc			889
Pro Val Ile Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly His Phe			
240 245 250			

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Ile	Tyr	Lys	Asn	Val	Ser	Glu	Asp	Leu	Pro	Leu	Pro	Thr	Phe	Ser	Pro	
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aca	ctg	ctg	ggg	gac	tcc	cgc	atg	ctg	tac	ttc	tgg	ttc	tct	gag	cga	985
Thr	Leu	Leu	Gly	Asp	Ser	Arg	Met	Leu	Tyr	Phe	Trp	Phe	Ser	Glu	Arg	
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Val	Phe	His	Ser	Leu	Ala	Lys	Val	Ala	Phe	Gln	Asp	Gly	Arg	Leu	Met	
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Leu	Ser	Leu	Met	Gly	Asp	Glu	Phe	Lys	Ala	Val	Leu	Glu	Thr	Trp	Gly	
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ttc	aac	acc	aac	cag	gaa	atc	ttc	caa	gag	gtt	gtc	ggc	ggc	ttc	ccc	1129
Phe	Asn	Thr	Asn	Gln	Glu	Ile	Phe	Gln	Glu	Val	Val	Gly	Gly	Phe	Pro	
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agc	cag	gcc	caa	gtc	acc	gtc	cac	tgc	ctc	aag	atg	ccc	aag	atc	tcc	1177
Ser	Gln	Ala	Gln	Val	Thr	Val	His	Cys	Leu	Lys	Met	Pro	Lys	Ile	Ser	
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tgc	caa	aac	aag	gga	gtc	gtg	gtc	aat	tct	tca	gtg	atg	gtg	aaa	ttc	1225
Cys	Gln	Asn	Lys	Gly	Val	Val	Val	Asn	Ser	Ser	Val	Met	Val	Lys	Phe	
	350				355					360					365	
ctc	ttt	cca	cgc	cca	gac	cag	caa	cat	tct	gta	gct	tac	aca	ttt	gaa	1273
Leu	Phe	Pro	Arg	Pro	Asp	Gln	Gln	His	Ser	Val	Ala	Tyr	Thr	Phe	Glu	
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Glu	Asp	Ile	Val	Thr	Thr	Val	Gln	Ala	Ser	Tyr	Ser	Lys	Lys	Lys	Leu	
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Phe	Leu	Ser	Leu	Leu	Asp	Phe	Gln	Ile	Thr	Pro	Lys	Thr	Val	Ser	Asn	
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Leu	Thr	Glu	Ser	Ser	Ser	Glu	Ser	Ile	Gln	Ser	Phe	Leu	Gln	Ser	Met	
	415					420					425					
atc	acc	gct	gtg	ggc	atc	cct	gag	gtc	atg	tct	cgg	ctc	gag	gta	gtg	1465
Ile	Thr	Ala	Val	Gly	Ile	Pro	Glu	Val	Met	Ser	Arg	Leu	Glu	Val	Val	
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ttt	aca	gcc	ctc	atg	aac	agc	aaa	ggc	gtg	agc	ctc	ttc	gac	atc	atc	1513
Phe	Thr	Ala	Leu	Met	Asn	Ser	Lys	Gly	Val	Ser	Leu	Phe	Asp	Ile	Ile	
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aac	cct	gag	att	atc	act	cga	gat	ggc	ttc	ctg	ctg	ctg	cag	atg	gac	1561
Asn	Pro	Glu	Ile	Ile	Thr	Arg	Asp	Gly	Phe	Leu	Leu	Leu	Gln	Met	Asp	
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Phe Gly Phe Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
480 485 490

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FOR REFERENCE